



## SEQUENCE LISTING

<110> Soto, Ana M.  
Sonnenschein, Carlos  
Geck, Peter  
Szelei, Jozsef

<120> A NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL PROLIFERATION AND USES THEREOF

<130> 24815-526

<140> US 09/512,581  
<141> 2000-02-24

<150> US 60/121,461  
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<170> PatentIn Ver. 2.0

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Ala Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys			
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Ser Glu Leu Ala Ser Gln Asn Lys Pro Leu Trp Gln Cys Tyr Leu Gly  
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Arg Phe Asn Asp Ile His Val Pro Ile Arg Leu Glu Cys Val Lys Phe  
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Ala Ala Gly Ser Ala Ile Val Lys Leu Ala Gln Glu Pro Cys Tyr His  
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Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile Asn  
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Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His Lys  
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Gly Leu Ser Arg Leu Arg Leu Pro Leu Glu Tyr Met Ala Ile Cys Ala  
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Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg Gln  
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Cys Leu Val Lys Asn Ile Asn Val Arg Arg Glu Tyr Leu Lys Gln His  
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Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val Val  
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Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys Val  
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Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe Val  
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Leu Glu Ile Leu Met Ala Lys Asn Glu Asn Asn Ser His Ala Phe Ile  
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Arg Lys Met Val Glu Asn Ile Lys Gln Thr Lys Asp Ala Gln Gly Pro  
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Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser Pro  
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 Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe Phe  
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 Lys Gly Ser Lys Lys Ser Gly Pro Pro Ala Pro Glu Glu Glu  
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1	5							10					15			

  

cct	ggg	gtc	aag	gaa	ata	tca	gat	aaa	ata	tct	aaa	gag	gag	atg	gtg	96
Pro	Gly	Val	Lys	Glu	Ile	Ser	Asp	Lys	Ile	Ser	Lys	Glu	Glu	Met	Val	
					20				25				30			

  

aga	cga	tta	aag	atg	gtt	gtg	aaa	act	ttt	atg	gat	atg	gac	cag	gac	144
Arg	Arg	Leu	Lys	Met	Val	Val	Lys	Thr	Phe	Met	Asp	Met	Asp	Gln	Asp	
					35			40				45				

  

tct	gaa	gaa	aag	gag	ctt	tat	tta	aac	cta	gct	tta	cat	ctt	gct	192	
Ser	Glu	Glu	Glu	Lys	Glu	Leu	Tyr	Leu	Asn	Leu	Ala	Leu	His	Leu	Ala	
					50		55			60						

  

tca	gat	ttt	ttt	ctc	aag	cat	cct	ggt	aaa	gat	gtt	cgc	tta	ctg	gta	240
Ser	Asp	Phe	Phe	Leu	Lys	His	Pro	Gly	Lys	Asp	Val	Arg	Leu	Leu	Val	
					65		70			75		80				

  

gcc	tgc	tgc	ctt	gct	gat	att	ttc	agg	att	tat	gct	cct	gaa	gct	cct	288
Ala	Cys	Cys	Leu	Ala	Asp	Ile	Phe	Arg	Ile	Tyr	Ala	Pro	Glu	Ala	Pro	
					85				90			95				

  

tac	aca	tcc	cct	gat	aaa	cta	aag	gat	ata	ttt	atg	ttt	ata	aca	aga	336
Tyr	Thr	Ser	Pro	Asp	Lys	Leu	Lys	Asp	Ile	Phe	Met	Phe	Ile	Thr	Arg	
					100			105			110					

  

cag	ttg	aag	ggg	cta	gag	gat	aca	aag	agc	cca	caa	ttc	aat	agg	tat	384
Gln	Leu	Lys	Gly	Leu	Glu	Asp	Thr	Lys	Ser	Pro	Gln	Phe	Asn	Arg	Tyr	
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Phe	Tyr	Leu	Leu	Glu	Asn	Ile	Ala	Trp	Val	Lys	Ser	Tyr	Asn	Ile	Cys	
					130		135			140						

  

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Phe	Glu	Leu	Glu	Asp	Ser	Asn	Glu	Ile	Phe	Thr	Gln	Leu	Tyr	Arg	Thr	
					145		150			155		160				

  

tta	ttt	tca	gtt	ata	aac	aat	ggc	cac	aat	cag	aaa	gtc	cat	atg	cac	528
Leu	Phe	Ser	Val	Ile	Asn	Asn	Gly	His	Asn	Gln	Lys	Val	His	Met	His	
					165			170			175					

atg gta gac ctt atg agc tct att att tgt gaa ggt gat aca gtg tct		576	
Met Val Asp Leu Met Ser Ser Ile Ile Cys Glu Gly Asp Thr Val Ser			
180	185	190	
cag gag ctt ttg gat acg gtt tta gta aat ctg gta cct gct cat aag		624	
Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His Lys			
195	200	205	
aat tta aac aag caa gca tat gat ttg gca aag gct tta ctg aag agg		672	
Asn Leu Asn Lys Gln Ala Tyr Asp Leu Ala Lys Ala Leu Leu Lys Arg			
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aca gct caa gct att gag cca tat att acc act ttt ttt aat cag gtt		720	
Thr Ala Gln Ala Ile Glu Pro Tyr Ile Thr Thr Phe Phe Asn Gln Val			
225	230	235	240
ctg atg ctt ggg aaa aca tct atc agc gat ttg tca gag cat gtc ttt		768	
Leu Met Leu Gly Lys Thr Ser Ile Ser Asp Leu Ser Glu His Val Phe			
245	250	255	
gac tta att ttg gag ctc tac aat att gat agt cat ttg ctg ctc tct		816	
Asp Leu Ile Leu Glu Leu Tyr Asn Ile Asp Ser His Leu Leu Leu Ser			
260	265	270	
gtt tta ccc cag ctt gaa ttt aaa tta aag agc aat gat aat gag gag		864	
Val Leu Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Asn Glu Glu			
275	280	285	
cgc cta caa gtt gtt aaa cta ctg gca aaa atg ttt ggg gca aag gat		912	
Arg Leu Gln Val Val Lys Leu Leu Ala Lys Met Phe Gly Ala Lys Asp			
290	295	300	
tca gaa ttg gct tct caa aac aag cca ctt tgg cag tgc tac ttg ggc		960	
Ser Glu Leu Ala Ser Gln Asn Lys Pro Leu Trp Gln Cys Tyr Leu Gly			
305	310	315	320
agg ttt aat gat atc cat gta cca atc cgc ctg gaa tgt gtg aaa ttt		1008	
Arg Phe Asn Asp Ile His Val Pro Ile Arg Leu Glu Cys Val Lys Phe			
325	330	335	
gct agc cat tgt ctc atg aac cat cct gat tta gca aaa gac tta aca		1056	
Ala Ser His Cys Leu Met Asn His Pro Asp Leu Ala Lys Asp Leu Thr			
340	345	350	
gag tat ctt aaa gtg agg tca cat gac cct gag gaa gct att aga cat		1104	
Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg His			
355	360	365	
gat gtt att gtg tca ata gtt aca gct gct aaa aag gat att ctt ctg		1152	
Asp Val Ile Val Ser Ile Val Thr Ala Ala Lys Lys Asp Ile Leu Leu			
370	375	380	
gtc aat gat cac tta ctt aat ttt gtg aga gag aga aca tta gac aaa		1200	
Val Asn Asp His Leu Leu Asn Phe Val Arg Glu Arg Thr Leu Asp Lys			
385	390	395	400

cga tgg aga gta cgc aaa gaa gcc atg atg gga ctt gcc caa att tat Arg Trp Arg Val Arg Lys Glu Ala Met Met Gly Leu Ala Gln Ile Tyr 405 410 415	1248
aag aaa tat gct tta cag tca gca gct gga aaa gat gct gca aaa cag Lys Lys Tyr Ala Leu Gln Ser Ala Ala Gly Lys Asp Ala Ala Lys Gln 420 425 430	1296
ata gca tgg atc aaa gac aaa ttg cta cat ata tat tat caa aat agt Ile Ala Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn Ser 435 440 445	1344
att gat gat cga cta ctt gtt gaa cg <sup>g</sup> atc ttt gct caa tac atg gtt Ile Asp Asp Arg Leu Leu Val Glu Arg Ile Phe Ala Gln Tyr Met Val 450 455 460	1392
cct cac aat tta gaa act aca gaa cg <sup>g</sup> atg aaa tgc tta tat tac ttg Pro His Asn Leu Glu Thr Thr Glu Arg Met Lys Cys Leu Tyr Tyr Leu 465 470 475 480	1440
tat gcc aca ctg gat tta aat gct gtg aaa gca ttg aat gaa atg tgg Tyr Ala Thr Leu Asp Leu Asn Ala Val Lys Ala Leu Asn Glu Met Trp 485 490 495	1488
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gaa ggt tgt gtg cgt gaa ata act aag aag ttg ggc aac ccc aaa cag Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys Gln 580 585 590	1776
cct aca aat cct ttc ctg gaa atg atc aag ttt ctc ttg gag agg ata Pro Thr Asn Pro Phe Leu Glu Met Ile Lys Phe Leu Leu Glu Arg Ile 595 600 605	1824
gca cct gtg cac ata gat acc gaa tct atc agt gct ctt att aaa caa Ala Pro Val His Ile Asp Thr Glu Ser Ile Ser Ala Leu Ile Lys Gln 610 615 620	1872
gtg aac aaa tca ata gat gga aca gca gat gat gaa gat gag ggt gtt	1920

Val Asn Lys Ser Ile Asp Gly Thr Ala Asp Asp Glu Asp Glu Gly Val			
625	630	635	640
cca act gat caa gcc atc aga gca ggt ctt gaa ctg ctt aag gta ctc			1968
Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val Leu			
645	650	655	
tca ttt aca cat ccc atc tca ttt cat tct gct gaa aca ttt gaa tca			2016
Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu Ser			
660	665	670	
tta ctg gct tgt ctg aaa atg gat gat gaa aaa gta gca gaa gct gca			2064
Leu Leu Ala Cys Leu Lys Met Asp Asp Glu Lys Val Ala Glu Ala Ala			
675	680	685	
cta caa att ttc aaa aac aca gga agc aaa att gaa gag gat ttt cca			2112
Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe Pro			
690	695	700	
cac atc aga tca gcc ttg ctt cct gtt tta cat cac aaa tct aaa aaa			2160
His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys Lys			
705	710	715	720
gga ccc ccc cgt caa gcc aaa tat gcc att cat tgt atc cat gcg ata			2208
Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala Ile			
725	730	735	
ttt tct agt aaa gag acc cag ttt gca cag ata ttt gag cct ctg cat			2256
Phe Ser Ser Lys Glu Thr Gln Phe Ala Gln Ile Phe Glu Pro Leu His			
740	745	750	
aag agc cta gat cca agc aac ctg gaa cat ctc ata aca cca ttg gtt			2304
Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu Val			
755	760	765	
act att ggt cat att gct ctc ctt gca cct gat caa ttt gct gct cct			2352
Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala Pro			
770	775	780	
tgg aaa tct tgg gta gct act ttc att gtg aaa gat ctt ctc atg aat			2400
Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met Asn			
785	790	795	800
gat cgg ctt cca ggg aaa aag aca act aaa ctt tgg gtt cca gat gaa			2448
Asp Arg Leu Pro Gly Lys Lys Thr Thr Lys Leu Trp Val Pro Asp Glu			
805	810	815	
gaa gta tct cct gag aca atg gtc aaa att cag gct att aaa atg atg			2496
Glu Val Ser Pro Glu Thr Met Val Lys Ile Gln Ala Ile Lys Met Met			
820	825	830	
gtt cga tgg cta ctt gga atg aaa aat aat cac agt aaa tca gga act			2544
Val Arg Trp Leu Leu Gly Met Lys Asn Asn His Ser Lys Ser Gly Thr			
835	840	845	
tct acc tta aga ttg cta aca aca ata ttg cat agt gat gga gac ttg			2592
Ser Thr Leu Arg Leu Leu Thr Thr Ile Leu His Ser Asp Gly Asp Leu			

850	855	860	
aca gaa cag ggg aaa att agt aaa cca gat atg tca cgt ctg aga ctt Thr Glu Gln Gly Lys Ile Ser Lys Pro Asp Met Ser Arg Leu Arg Leu 865 870 875 880			2640
gct gct ggg agt gct att gtg aag ctg gca caa gaa ccc tgt tac cat Ala Ala Gly Ser Ala Ile Val Lys Leu Ala Gln Glu Pro Cys Tyr His 885 890 895			2688
gaa atc atc aca tta gaa caa tat cag cta tgt gca tta gct atc aac Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile Asn 900 905 910			2736
gat gaa tgc tat caa gta aga caa gtg ttt gcc cag aaa ctt cac aaa Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His Lys 915 920 925			2784
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ctt tgt gca aaa gat cct gta aag gag aga aga gct cat gct agg caa Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg Gln 945 950 955 960			2880
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gca gct gtt agt gaa aaa tta ttg tct ctt cta cca gag tat gtt gtt Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val Val 980 985 990			2976
cca tat aca att cac ctt ttg gca cat gac cca gat tat gtc aaa gta Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys Val 995 1000 1005			3024
cag gat att gaa caa ctt aaa gat gtt aaa gaa tgt ctt tgg ttt gtt Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe Val 1010 1015 1020			3072
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gat gat gca aaa atg aat gaa aaa ctg tac act gtg tgt gat gtt gcc Asp Asp Ala Lys Met Asn Glu Lys Leu Tyr Thr Val Cys Asp Val Ala 1060 1065 1070			3216
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cca ctt tca tca gca ggc aag caa tct cag acc aaa tca tca cga atg Pro Leu Ser Ser Ala Gly Lys Gln Ser Gln Thr Lys Ser Ser Arg Met 1140                   1145                   1150	3456
gaa act gta agc aat gca agc agc tca aat cca agc tct cct gga Glu Thr Val Ser Asn Ala Ser Ser Ser Asn Pro Ser Ser Pro Gly 1155                   1160                   1165	3504
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gac ttg act aag ttg gta cag gaa cag aaa cct aaa ggc agt cag cga Asp Leu Thr Lys Leu Val Gln Glu Gln Lys Pro Lys Gly Ser Gin Arg 1235                   1240                   1245	3744
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cct gag gaa aag agg ctc aaa gaa gat ata tta gaa aat gaa gat gaa Pro Glu Glu Lys Arg Leu Lys Glu Asp Ile Leu Glu Asn Glu Asp Glu 1265                   1270                   1275                   1280	3840
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Lys Gly Ser Lys Lys Ser Gly Pro Pro Ala Pro Glu Glu Glu  
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Gln His Arg Val Ser Arg Arg Ala Gln Gln Arg Ala Glu Ser Pro Glu  
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Met Ala His Ser Lys Thr Arg Thr  
1 5

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gat ata ttt atg ttt ata aca aga cag ttg aag ggg cta gag gat aca Asp Ile Phe Met Phe Ile Thr Arg Gln Leu Lys Gly Leu Glu Asp Thr 105	110	115	509
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tgg gtc aag tca tat aac ata tgc ttt gag tta gaa gat agc aat gaa Trp Val Lys Ser Tyr Asn Ile Cys Phe Glu Leu Glu Asp Ser Asn Glu 140	145	150	605
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cac aat cag aaa gtc cat atg cac atg gta gac ctt atg agc tct att His Asn Gln Lys Val His Met Val Asp Leu Met Ser Ser Ile 170	175	180	701
att tgt gaa ggt gat aca gtg tct cag gag ctt ttg gat acg gtt tta Ile Cys Glu Gly Asp Thr Val Ser Gln Glu Leu Leu Asp Thr Val Leu 185	190	195	749
195	200		
gta aat ctg gta cct gct cat aag aat tta aac aag caa gca tat gat Val Asn Leu Val Pro Ala His Lys Asn Leu Asn Lys Gln Ala Tyr Asp 205	210	215	797
215			
ttg gca aag gct tta ctg aag agg aca gct caa gct att gag cca tat Leu Ala Lys Ala Leu Leu Lys Arg Thr Ala Gln Ala Ile Glu Pro Tyr 220	225	230	845
230			
att acc act ttt ttt aat cag gtt ctg atg ctt ggg aaa aca tct atc Ile Thr Thr Phe Phe Asn Gln Val Leu Met Leu Gly Lys Thr Ser Ile 235	240	245	893
245			
agc gat ttg tca gag cat gtc ttt gac tta att ttg gag ctc tac aat Ser Asp Leu Ser Glu His Val Phe Asp Leu Ile Leu Glu Leu Tyr Asn 250	255	260	941
260			
att gat agt cat ttg ctg ctc tct gtt tta ccc cag ctt gaa ttt aaa Ile Asp Ser His Leu Leu Leu Ser Val Leu Pro Gln Leu Glu Phe Lys 265	270	275	989
275	280		
tta aag agc aat gat aat gag gag cgc cta caa gtt gtt aaa cta ctg Leu Lys Ser Asn Asp Asn Glu Glu Arg Leu Gln Val Val Lys Leu Leu 285	290	295	1037
295			
gca aaa atg ttt ggg gca aag gat tca gaa ttg gct tct caa aac aag Ala Lys Met Phe Gly Ala Lys Asp Ser Glu Leu Ala Ser Gln Asn Lys 300	305	310	1085
310			

cca ctt tgg cag tgc tac ttg ggc agg ttt aat gat atc cat gta cca		1133	
Pro Leu Trp Gln Cys Tyr Leu Gly Arg Phe Asn Asp Ile His Val Pro			
315	320	325	
atc cgc ctg gaa tgt gtg aaa ttt gct agc cat tgt ctc atg aac cat		1181	
Ile Arg Leu Glu Cys Val Lys Phe Ala Ser His Cys Leu Met Asn His			
330	335	340	
cct gat tta gca aaa gac tta aca gag tat ctt aaa gtg agg tca cat		1229	
Pro Asp Leu Ala Lys Asp Leu Thr Glu Tyr Leu Lys Val Arg Ser His			
345	350	355	360
gac cct gag gaa gct att aga cat gat gtt att gtg tca ata gtt aca		1277	
Asp Pro Glu Glu Ala Ile Arg His Asp Val Ile Val Ser Ile Val Thr			
365	370	375	
gct gct aaa aag gat att ctt ctg gtc aat gat cac tta ctt aat ttt		1325	
Ala Ala Lys Lys Asp Ile Leu Leu Asn Asp His Leu Leu Asn Phe			
380	385	390	
gtg aga gag aga aca tta gac aaa cga tgg aga gta cgc aaa gaa gcc		1373	
Val Arg Glu Arg Thr Leu Asp Lys Arg Trp Arg Val Arg Lys Glu Ala			
395	400	405	
atg atg gga ctt gcc caa att tat aag aaa tat gct tta cag tca gca		1421	
Met Met Gly Leu Ala Gln Ile Tyr Lys Tyr Ala Leu Gln Ser Ala			
410	415	420	
gct gga aaa gat gct gca aaa cag ata gca tgg atc aaa gac aaa ttg		1469	
Ala Gly Lys Asp Ala Ala Lys Gln Ile Ala Trp Ile Lys Asp Lys Leu			
425	430	435	440
cta cat ata tat tat caa aat agt att gat gat cga cta ctt gtt gaa		1517	
Leu His Ile Tyr Tyr Gln Asn Ser Ile Asp Asp Arg Leu Leu Val Glu			
445	450	455	
cg <sup>g</sup> atc ttt gct caa tac atg gtt cct cac aat tta gaa act aca gaa		1565	
Arg Ile Phe Ala Gln Tyr Met Val Pro His Asn Leu Glu Thr Thr Glu			
460	465	470	
cg <sup>g</sup> atg aaa tgc tta tat tac ttg tat gcc aca ctg gat tta aat gct		1613	
Arg Met Lys Cys Leu Tyr Tyr Ala Thr Leu Asp Leu Asn Ala			
475	480	485	
gtg aaa gca ttg aat gaa atg tgg aaa tgt caa aat ctg ctc cga cat		1661	
Val Lys Ala Leu Asn Glu Met Trp Lys Cys Gln Asn Leu Leu Arg His			
490	495	500	
caa gta aag gat ttg ctt gac ttg att aag caa ccc aaa aca gat gcc		1709	
Gln Val Lys Asp Leu Leu Asp Leu Ile Lys Gln Pro Lys Thr Asp Ala			
505	510	515	520
agt gtc aag gcc ata ttt tca aaa gtg atg gtt att aca aga aat tta		1757	
Ser Val Lys Ala Ile Phe Ser Lys Val Met Val Ile Thr Arg Asn Leu			
525	530	535	

cct gat cct ggt aag gct cag gat ttc atg aag aaa ttc aca cag gtg Pro Asp Pro Gly Lys Ala Gln Asp Phe Met Lys Lys Phe Thr Gln Val 540 545 550	1805
tta gaa gat gat gag aaa ata aga aag cag tta gaa gta ctt gtt agt Leu Glu Asp Asp Glu Lys Ile Arg Lys Gln Leu Glu Val Leu Val Ser 555 560 565	1853
cca aca tgc tcc tgc aag cag gct gaa ggt tgt gtg cgt gaa ata act Pro Thr Cys Ser Cys Lys Gln Ala Glu Gly Cys Val Arg Glu Ile Thr 570 575 580	1901
aag aag ttg ggc aac ccc aaa cag cct aca aat cct ttc ctg gaa atg Lys Lys Leu Gly Asn Pro Lys Gln Pro Thr Asn Pro Phe Leu Glu Met 585 590 595 600	1949
atc aag ttt ctc ttg gag agg ata gca cct gtg cac ata gat acc gaa Ile Lys Phe Leu Leu Glu Arg Ile Ala Pro Val His Ile Asp Thr Glu 605 610 615	1997
tct atc agt gct ctt att aaa caa gtg aac aaa tca ata gat gga aca Ser Ile Ser Ala Leu Ile Lys Gln Val Asn Lys Ser Ile Asp Gly Thr 620 625 630	2045
gca gat gat gaa gat gag ggt gtt cca act gat caa gcc atc aga gca Ala Asp Asp Glu Asp Gly Val Pro Thr Asp Gln Ala Ile Arg Ala 635 640 645	2093
ggc ctt gaa ctg ctt aag gta ctc tca ttt aca cat ccc atc tca ttt Gly Leu Glu Leu Leu Lys Val Leu Ser Phe Thr His Pro Ile Ser Phe 650 655 660	2141
cat tct gct gaa aca ttt gaa tca tta ctg gct tgt ctg aaa atg gat His Ser Ala Glu Thr Phe Glu Ser Leu Leu Ala Cys Leu Lys Met Asp 665 670 675 680	2189
gat gaa aaa gta gca gaa gct gca cta caa att ttc aaa aac aca gga Asp Glu Lys Val Ala Glu Ala Leu Gln Ile Phe Lys Asn Thr Gly 685 690 695	2237
agc aaa att gaa gag gat ttt cca cac atc aga tca gcc ttg ctt cct Ser Lys Ile Glu Glu Asp Phe Pro His Ile Arg Ser Ala Leu Leu Pro 700 705 710	2285
gtt tta cat cac aaa tct aaa aaa gga ccc ccc cgt caa gcc aaa tat Val Leu His His Lys Ser Lys Lys Gly Pro Pro Arg Gln Ala Lys Tyr 715 720 725	2333
gcc att cat tgt atc cat gcg ata ttt tct agt aaa gag acc cag ttt Ala Ile His Cys Ile His Ala Ile Phe Ser Ser Lys Glu Thr Gln Phe 730 735 740	2381
gca cag ata ttt gag cct ctg cat aag agc cta gat cca agc aac ctg Ala Gln Ile Phe Glu Pro Leu His Lys Ser Leu Asp Pro Ser Asn Leu 745 750 755 760	2429
gaa cat ctc ata aca cca ttg gtt act att ggt cat att gct ctc ctt	2477

Glu His Leu Ile Thr Pro Leu Val Thr Ile Gly His Ile Ala Leu Leu			
765	770	775	
gca cct gat caa ttt gct gct cct tgg aaa tct tgg gta gct act ttc			2525
Ala Pro Asp Gln Phe Ala Ala Pro Trp Lys Ser Trp Val Ala Thr Phe			
780	785	790	
att gtg aaa gat ctt ctc atg aat gat cgg ctt cca ggg aaa aag aca			2573
Ile Val Lys Asp Leu Leu Met Asn Asp Arg Leu Pro Gly Lys Lys Thr			
795	800	805	
act aaa ctt tgg gtt cca gat gaa gaa gta tct cct gag aca atg gtc			2621
Thr Lys Leu Trp Val Pro Asp Glu Glu Val Ser Pro Glu Thr Met Val			
810	815	820	
aaa att cag gct att aaa atg atg gtt cga tgg cta ctt gga atg aaa			2669
Lys Ile Gln Ala Ile Lys Met Met Val Arg Trp Leu Leu Gly Met Lys			
825	830	835	840
aat aat cac agt aaa tca gga act tct acc tta aga ttg cta aca aca			2717
Asn Asn His Ser Lys Ser Gly Thr Ser Thr Leu Arg Leu Leu Thr Thr			
845	850	855	
ata ttg cat agt gat gga gac ttg aca gaa cag ggg aaa att agt aaa			2765
Ile Leu His Ser Asp Gly Asp Leu Thr Glu Gln Gly Lys Ile Ser Lys			
860	865	870	
cca gat atg tca cgt ctg aga ctt gct gct ggg agt gct att gtg aag			2813
Pro Asp Met Ser Arg Leu Arg Leu Ala Ala Gly Ser Ala Ile Val Lys			
875	880	885	
ctg gca caa gaa ccc tgt tac cat gaa atc atc aca tta gaa caa tat			2861
Leu Ala Gln Glu Pro Cys Tyr His Glu Ile Ile Thr Leu Glu Gln Tyr			
890	895	900	
cag cta tgt gca tta gct atc aac gat gaa tgc tat caa gta aga caa			2909
Gln Leu Cys Ala Leu Ala Ile Asn Asp Glu Cys Tyr Gln Val Arg Gln			
905	910	915	920
gtg ttt gcc cag aaa ctt cac aaa ggc ctt tcc cgt tta cgg ctt cca			2957
Val Phe Ala Gln Lys Leu His Lys Gly Leu Ser Arg Leu Arg Leu Pro			
925	930	935	
ctt gag tat atg gca atc tgt gcc ctt tgt gca aaa gat cct gta aag			3005
Leu Glu Tyr Met Ala Ile Cys Ala Leu Cys Ala Lys Asp Pro Val Lys			
940	945	950	
gag aga aga gct cat gct agg caa tgt ttg gtg aaa aat ata aat gta			3053
Glu Arg Arg Ala His Ala Arg Gln Cys Leu Val Lys Asn Ile Asn Val			
955	960	965	
agg cgg gag tat ctg aag cag cat gca gct gtt agt gaa aaa tta ttg			3101
Arg Arg Glu Tyr Leu Lys Gln His Ala Ala Val Ser Glu Lys Leu Leu			
970	975	980	
tct ctt cta cca gag tat gtt gtt cca tat aca att cac ctt ttg gca			3149
Ser Leu Leu Pro Glu Tyr Val Val Pro Tyr Thr Ile His Leu Leu Ala			

985	990	995	1000	
cat gac cca gat tat gtc aaa gta cag gat att gaa caa ctt aaa gat His Asp Pro Asp Tyr Val Lys Val Gln Asp Ile Glu Gln Leu Lys Asp 1005		1010		3197
gtt aaa gaa tgt ctt tgg ttt gtt ctg gaa ata tta atg gct aaa aat Val Lys Glu Cys Leu Trp Phe Val Leu Glu Ile Leu Met Ala Lys Asn 1020	1025		1030	3245
gaa aat aac agt cac gct ttt atc aga aag atg gta gaa aat att aaa Glu Asn Asn Ser His Ala Phe Ile Arg Lys Met Val Glu Asn Ile Lys 1035	1040		1045	3293
caa aca aaa gat gcc caa gga cca gat gat gca aaa atg aat gaa aaa Gln Thr Lys Asp Ala Gln Gly Pro Asp Asp Ala Lys Met Asn Glu Lys 1050	1055		1060	3341
ctg tac act gtg tgt gat gtt gcc atg aat atc atc atg tca aag agt Leu Tyr Thr Val Cys Asp Val Ala Met Asn Ile Ile Met Ser Lys Ser 1065	1070	1075	1080	3389
act aca tac agt ttg gaa tct cct aaa gac ccg gta cta cca gct cgt Thr Thr Tyr Ser Leu Glu Ser Pro Lys Asp Pro Val Leu Pro Ala Arg 1085	1090		1095	3437
ttc ttc act caa cct gac aag aat ttc agt aac acc aaa aat tat ctg Phe Phe Thr Gln Pro Asp Lys Asn Phe Ser Asn Thr Lys Asn Tyr Leu 1100	1105		1110	3485
cct cct gaa atg aaa tca ttt ttc act cct gga aaa cct aaa aca acc Pro Pro Glu Met Lys Ser Phe Phe Thr Pro Gly Lys Pro Lys Thr Thr 1115	1120		1125	3533
aat gtt cta gga gct gtt aac aag cca ctt tca tca gca ggc aag caa Asn Val Leu Gly Ala Val Asn Lys Pro Leu Ser Ser Ala Gly Lys Gln 1130	1135		1140	3581
tct cag acc aaa tca tca cga atg gaa act gta agc aat gca agc agc Ser Gln Thr Lys Ser Ser Arg Met Glu Thr Val Ser Asn Ala Ser Ser 1145	1150	1155	1160	3629
agc tca aat cca agc tct cct gga aga ata aag ggg agg ctt gat agt Ser Ser Asn Pro Ser Ser Pro Gly Arg Ile Lys Gly Arg Leu Asp Ser 1165	1170		1175	3677
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ttg ccg ggg aaa aaa agt gac aag aga gac gac tct gat ctt gta agg Leu Pro Gly Lys Lys Ser Asp Lys Arg Asp Asp Ser Asp Leu Val Arg 1195	1200		1205	3773
tct gaa ttg gag aag cct aga ggc agg aaa aaa acg ccc gtc aca gaa Ser Glu Leu Glu Lys Pro Arg Gly Arg Lys Lys Thr Pro Val Thr Glu 1210	1215		1220	3821

cag gag gag aaa tta ggt atg gat gac ttg act aag ttg gta cag gaa 3869  
 Gln Glu Glu Lys Leu Gly Met Asp Asp Leu Thr Lys Leu Val Gln Glu  
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 1245 1250 1255

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 1260 1265 1270

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 Lys Arg Gly Arg Pro Pro Lys Pro Leu Gly Gly Thr Pro Lys Glu  
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 Thr Glu Gln Lys Ser Lys Gln His Arg Val Ser Arg Arg Ala  
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 Ser Gln Pro Lys Lys Asn Val  
 1385 1390

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<223> Description of Artificial Sequence: motif

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